

0219us410-sequence.txt  
SEQUENCE LISTING

<110> Maxygen Aps; Maxygen Holding  
 <120> Protein C or activated protein C-like molecules  
 <130> 0219us410 - protein C  
 <140>  
 <141>  
 <160> 40  
 <170> PatentIn Ver. 2.1  
 <210> 1  
 <211> 1383  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1383)  
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 <221> mat\_peptide  
 <222> (127)..(1383)

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 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile  
 -40 -35 -30  
 tcc ggc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt 96  
 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg  
 -25 -20 -15  
 gcc cac cag gtg ctg cgg atc cgc aaa cgt gcc aac tcc ttc ctg gag 144  
 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu  
 -10 -5 -1 1 5  
 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt 192  
 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys  
 10 15 20  
 gac ttc gag gag gcc aag gaa att ttc caa aat gtg gat gac aca ctg 240  
 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu  
 25 30 35  
 gcc ttc tgg tcc aag cac gtc gac ggt gac cag tgc ttg gtc ttg ccc 288  
 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro  
 40 45 50  
 ttg gag cac ccg tgc gcc agc ctg tgc tgc ggg cac ggc acg tgc atc 336  
 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile  
 55 60 65 70  
 gac ggc atc ggc agc ttc agc tgc gac tgc cgc agc ggc tgg gag ggc 384  
 Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly  
 75 80 85  
 cgc ttc tgc cag cgc gag gtg agc ttc ctg aat tgc tcg ctg gac aac 432  
 Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn  
 90 95 100  
 ggc ggc tgc acg cat tac tgc cta gag gag gtg ggc tgg cgg cgc tgt 480  
 Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys

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105	110	115	
agc tgt gcg cct ggc tac aag ctg ggg gac gac ctc ctg cag tgt cac Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His 120 125 130			528
ccc gca gtg aag ttc cct tgt ggg agg ccc tgg aag cgg atg gag aag Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys 135 140 145 150			576
aag cgc agt cac ctg aaa cga gac aca gaa gac caa gaa gac caa gta Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val 155 160 165			624
gat ccg cgg ctc att gat ggg aag atg acc agg cgg gga gac agc ccc Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro 170 175 180			672
tgg cag gtg gtc ctg ctg gac tca aag aag aag ctg gcc tgc ggg gca Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala 185 190 195			720
gtg ctc atc cac ccc tcc tgg gtg ctg aca gcg gcc cac tgc atg gat Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp 200 205 210			768
gag tcc aag aag ctc ctt gtc agg ctt gga gag tat gac ctg cgg cgc Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg 215 220 225 230			816
tgg gag aag tgg gag ctg gac ctg gac atc aag gag gtc ttc gtc cac Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His 235 240 245			864
ccc aac tac agc aag agc acc acc gac aat gac atc gca ctg ctg cac Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His 250 255 260			912
ctg gcc cag ccc gcc acc ctc tcg cag acc ata gtg ccc atc tgc ctc Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu 265 270 275			960
ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu 280 285 290			1008
acc ctc gtg acg ggc tgg ggc tac cac agc agc cga gag aag gag gcc Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala 295 300 305 310			1056
aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val 315 320 325			1104
ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn 330 335 340			1152
atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly 345 350 355			1200
gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu 360 365 370			1248
gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac			1296

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val Gly Leu val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr  
375 380 385 390

ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg atc cat ggg cac 1344  
Gly val Tyr Thr Lys val Ser Arg Tyr Leu Asp Trp Ile His Gly His  
395 400 405

atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct 1383  
Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro  
410 415

<210> 2  
<211> 461  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Trp Gln Leu Thr Ser Leu Leu Leu Phe val Ala Thr Trp Gly Ile  
-40 -35 -30

Ser Gly Thr Pro Ala Pro Leu Asp Ser val Phe Ser Ser Ser Glu Arg  
-25 -20 -15

Ala His Gln val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu  
-10 -5 -1 1 5

Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys  
10 15 20

Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn val Asp Asp Thr Leu  
25 30 35

Ala Phe Trp Ser Lys His val Asp Gly Asp Gln Cys Leu val Leu Pro  
40 45 50

Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile  
55 60 65 70

Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly  
75 80 85

Arg Phe Cys Gln Arg Glu val Ser Phe Leu Asn Cys Ser Leu Asp Asn  
90 95 100

Gly Gly Cys Thr His Tyr Cys Leu Glu Glu val Gly Trp Arg Arg Cys  
105 110 115

Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His  
120 125 130

Pro Ala val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys  
135 140 145 150

Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln val  
155 160 165

Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro  
170 175 180

Trp Gln val val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala  
185 190 195

val Leu Ile His Pro Ser Trp val Leu Thr Ala Ala His Cys Met Asp  
200 205 210

Glu Ser Lys Lys Leu Leu val Arg Leu Gly Glu Tyr Asp Leu Arg Arg

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215                      220                      225                      230

Trp Glu Lys Trp Glu<sub>235</sub> Leu Asp Leu Asp Ile<sub>240</sub> Lys Glu Val Phe Val<sub>245</sub> His

Pro Asn Tyr Ser<sub>250</sub> Lys Ser Thr Thr Asp<sub>255</sub> Asn Asp Ile Ala Leu<sub>260</sub> Leu His

Leu Ala Gln Pro Ala Thr Leu Ser<sub>270</sub> Gln Thr Ile Val Pro<sub>275</sub> Ile Cys Leu

Pro Asp<sub>280</sub> Ser Gly Leu Ala Glu<sub>285</sub> Arg Glu Leu Asn Gln<sub>290</sub> Ala Gly Gln Glu

Thr<sub>295</sub> Leu Val Thr Gly Trp<sub>300</sub> Gly Tyr His Ser Ser<sub>305</sub> Arg Glu Lys Glu Ala<sub>310</sub>

Lys Arg Asn Arg Thr<sub>315</sub> Phe Val Leu Asn Phe<sub>320</sub> Ile Lys Ile Pro Val<sub>325</sub> Val

Pro His Asn Glu<sub>330</sub> Cys Ser Glu Val Met<sub>335</sub> Ser Asn Met Val<sub>340</sub> Ser Glu Asn

Met Leu Cys<sub>345</sub> Ala Gly Ile Leu Gly<sub>350</sub> Asp Arg Gln Asp Ala<sub>355</sub> Cys Glu Gly

Asp Ser Gly Gly Pro Met Val<sub>365</sub> Ala Ser Phe His Gly<sub>370</sub> Thr Trp Phe Leu

Val<sub>375</sub> Gly Leu Val Ser Trp<sub>380</sub> Gly Glu Gly Cys Gly<sub>385</sub> Leu Leu His Asn Tyr<sub>390</sub>

Gly Val Tyr Thr Lys<sub>395</sub> Val Ser Arg Tyr Leu<sub>400</sub> Asp Trp Ile His Gly<sub>405</sub> His

Ile Arg Asp Lys Glu Ala Pro Gln Lys<sub>415</sub> Ser Trp Ala Pro

<210> 3  
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 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1257)

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 Ala Asn Ser Phe Leu<sub>5</sub> Glu Glu Leu Arg His<sub>10</sub> Ser Ser Leu Glu Arg<sub>15</sub> Glu

tgc ata gag gag atc tgt gac ttc gag gag gcc aag gaa att ttc caa 96  
 Cys Ile Glu Glu<sub>20</sub> Ile Cys Asp Phe Glu<sub>25</sub> Glu Ala Lys Glu Ile<sub>30</sub> Phe Gln

aat gtg gat gac aca ctg gcc ttc tgg tcc aag cac gtc gac ggt gac 144  
 Asn Val Asp<sub>35</sub> Asp Thr Leu Ala Phe<sub>40</sub> Trp Ser Lys His Val<sub>45</sub> Asp Gly Asp

cag tgc ttg gtc ttg ccc ttg gag cac ccg tgc gcc agc ctg tgc tgc 192  
 Gln Cys<sub>50</sub> Leu Val Leu Pro Leu<sub>55</sub> Glu His Pro Cys Ala<sub>60</sub> Ser Leu Cys Cys

ggg cac ggc acg tgc atc gac ggc atc ggc agc ttc agc tgc gac tgc 240

Gly 65	His	Gly	Thr	Cys	Ile 70	Asp	Gly	Ile	Gly	Ser 75	Phe	Ser	Cys	Asp	Cys 80	
cgc Arg	agc Ser	ggc Gly	tgg Trp	gag Glu 85	ggc Gly	cgc Arg	ttc Phe	tgc Cys	cag Gln 90	cgc Arg	gag Glu	gtg Val	agc Ser	ttc Phe 95	ctc Leu	288
aat Asn	tgc Cys	tcg Ser	ctg Leu 100	gac Asp	aac Asn	ggc Gly	ggc Gly	tgc Cys 105	acg Thr	cat His	tac Tyr	tgc Cys	cta Leu 110	gag Glu	gag Glu	336
gtg Val	ggc Gly	tgg Trp 115	cgg Arg	cgc Arg	tgt Cys	agc Ser	tgt Cys 120	gcg Ala	cct Pro	ggc Gly	tac Tyr	aag Lys 125	ctg Leu	ggg Gly	gac Asp	384
gac Asp	ctc Leu 130	ctg Leu	cag Gln	tgt Cys	cac His	ccc Pro 135	gca Ala	gtg Val	aag Lys	ttc Phe	cct Pro 140	tgt Cys	ggg Gly	agg Arg	ccc Pro	432
tgg Trp 145	aag Lys	cgg Arg	atg Met	gag Glu	aag Lys 150	aag Lys	cgc Arg	agt Ser	cac His	ctg Leu 155	aaa Lys	cga Arg	gac Asp	aca Thr	gaa Glu 160	480
gac Asp	caa Gln	gaa Glu	gac Asp	caa Gln 165	gta Val	gat Asp	ccg Pro	cgg Arg	ctc Leu 170	att Ile	gat Asp	ggg Gly	aag Lys	atg Met 175	acc Thr	528
agg Arg	cgg Arg	gga Gly	gac Asp 180	agc Ser	ccc Pro	tgg Trp	cag Gln	gtg Val 185	gtc Val	ctg Leu	ctg Leu	gac Asp	tca Ser 190	aag Lys	aag Lys	576
aag Lys	ctg Leu	gcc Ala 195	tgc Cys	ggg Gly	gca Ala	gtg Val	ctc Leu 200	atc Ile	cac His	ccc Pro	tcc Ser	tgg Trp 205	gtg Val	ctg Leu	aca Thr	624
gcg Ala	gcc Ala 210	cac His	tgc Cys	atg Met	gat Asp	gag Glu 215	tcc Ser	aag Lys	aag Lys	ctc Leu	ctt Leu 220	gtc Val	agg Arg	ctt Leu	gga Gly	672
gag Glu 225	tat Tyr	gac Asp	ctg Leu	cgg Arg	cgc Arg 230	tgg Trp	gag Glu	aag Lys	tgg Trp	gag Glu 235	ctg Leu	gac Asp	ctg Leu	gac Asp	atc Ile 240	720
aag Lys	gag Glu	gtc Val	ttc Phe	gtc Val 245	cac His	ccc Pro	aac Asn	tac Tyr	agc Ser 250	aag Lys	agc Ser	acc Thr	acc Thr	gac Asp 255	aat Asn	768
gac Asp	atc Ile	gca Ala	ctg Leu 260	ctg Leu	cac His	ctg Leu	gcc Ala	cag Gln 265	ccc Pro	gcc Ala	acc Thr	ctc Leu	tcg Ser 270	cag Gln	acc Thr	816
ata Ile	gtg Val	ccc Pro 275	atc Ile	tgc Cys	ctc Leu	ccg Pro	gac Asp 280	agc Ser	ggc Gly	ctt Leu	gca Ala	gag Glu 285	cgc Arg	gag Glu	ctc Leu	864
aat Asn	cag Gln 290	gcc Ala	ggc Gly	cag Gln	gag Glu	acc Thr 295	ctc Leu	gtg Val	acg Thr	ggc Gly	tgg Trp 300	ggc Gly	tac Tyr	cac His	agc Ser	912
agc Ser 305	cga Arg	gag Glu	aag Lys	gag Glu	gcc Ala 310	aag Lys	aga Arg	aac Asn	cgc Arg	acc Thr 315	ttc Phe	gtc Val	ctc Leu	aac Asn	ttc Phe 320	960
atc Ile	aag Lys	att Ile	ccc Pro	gtg Val 325	gtc Val	ccg Pro	cac His	aat Asn	gag Glu 330	tgc Cys	agc Ser	gag Glu	gtc Val	atg Met 335	agc Ser	1008

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aac atg gtg tct gag aac atg ctg tgt gcg ggc atc ctc ggg gac cgg 1056  
 Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg  
 340 345 350

cag gat gcc tgc gag ggc gac agt ggg ggg ccc atg gtc gcc tcc ttc 1104  
 Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe  
 355 360 365

cac ggc acc tgg ttc ctg gtg ggc ctg gtg agc tgg ggt gag ggc tgt 1152  
 His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys  
 370 375 380

ggg ctc ctt cac aac tac ggc gtt tac acc aaa gtc agc cgc tac ctc 1200  
 Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu  
 385 390 395 400

gac tgg atc cat ggg cac atc aga gac aag gaa gcc ccc cag aag agc 1248  
 Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser  
 405 410 415

tgg gca cct 1257  
 Trp Ala Pro

<210> 4  
 <211> 419  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Ala Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Leu Glu Arg Glu  
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Cys Ile Glu Glu Ile Cys Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln  
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Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp  
 35 40 45

Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser Leu Cys Cys  
 50 55 60

Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys  
 65 70 75 80

Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu  
 85 90 95

Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu  
 100 105 110

Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp  
 115 120 125

Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro  
 130 135 140

Trp Lys Arg Met Glu Lys Lys Arg Ser His Leu Lys Arg Asp Thr Glu  
 145 150 155 160

Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr  
 165 170 175

Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys  
 180 185 190

Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr

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195 200 205

Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Gly  
 210 215 220

Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile  
 225 230 235 240

Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn  
 245 250 255

Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr  
 260 265 270

Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu  
 275 280 285

Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly Tyr His Ser  
 290 295 300

Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe  
 305 310 315 320

Ile Lys Ile Pro Val Val Pro His Asn Glu Cys Ser Glu Val Met Ser  
 325 330 335

Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg  
 340 345 350

Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe  
 355 360 365

His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys  
 370 375 380

Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu  
 385 390 395 400

Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser  
 405 410 415

Trp Ala Pro

<210> 5  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
 caagtagatc cgcggctcat taacgggaag atgaccaggc gggg

44

<210> 6  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 6

<210> 7  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 ctgacagcgg cccactgcat gaacgagtcc aagaagctcc ttgtc

45

<210> 8  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 gacaaggagc ttcttgact cgttcatgca gtgggccgct gtcag

45

<210> 9  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 ctgacagcgg cccactgcat ggccgagtcc aagaagctcc ttgtc

45

<210> 10  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 10  
 gacaaggagc ttcttgact cgcccatgca gtgggccgct gtcag

45

<210> 11  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 11  
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46

<210> 12  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Primer

<400> 12  
gatgtcattg tcggtggtgc tgttgctgta gttggggtgg acgaag 46

<210> 13  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cgtccacccc aactacagca agaacaccac cgacaatgac atcgc 45

<210> 14  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
gcgatgtcat tgctggtggt gttcttgctg tagttggggt ggacg 45

<210> 15  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
ccctcgtgac gggctggggc aaccacagca gccgagagaa ggaggcc 47

<210> 16  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
ggcctccttc tctcggctgc tgtggttgcc ccagcccgtc acgaggg 47

<210> 17  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
cagcgaggtc atgagcaaca acgtgtctga gaacatgc 38

<210> 18

<211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 18  
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 <210> 19  
 <211> 39  
 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
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 <210> 20  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 20  
 gcatgttctc agacacggcg ttgctcatga cctcgctgc 39  
  
 <210> 21  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 21  
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 <210> 22  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
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 <210> 23  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer

<400> 23  
cccctggcag gtggtcctgc tgaactcaac caagaagctg gcctgcgggg 50

<210> 24  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
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<210> 25  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
ggcaggtggc cctgctggac aacaagacca agctggcctg cggggcagt 49

<210> 26  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
gcactgcccc gcaggccagc ttggtcttgt tgtccagcag gaccacctgc c 51

<210> 27  
<211> 42  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
gtcctgctgg actcaaaca gaccctggcc tgcggggcag tg 42

<210> 28  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 28  
cactgccccg caggccaggg tcttggttga gtccagcagg ac 42

<210> 29  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

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<210> 30

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

ggtcatactc tccaagcctg acaagggctt tgttggactc atccatgc 48

<210> 31

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ccaactacag caagagcaac accaccaatg acatcgact gctgcacctg 50

<210> 32

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 33

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

ggctggggct accacagcaa ccgaaccaag gaggccaaaga gaaaccgc 48

<210> 34

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

gcggtttctc ttggcctcct tggttcggtt gctgtggtag cccagcc 48

<210> 35  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 35  
 ggctaccaca gcagccgaaa caagaccgcc aagagaaacc gcaccttcg 49

<210> 36  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 36  
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<210> 37  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 37  
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<210> 38  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 38  
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<210> 39  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 39  
 ggtgagctgg ggtgagggct gtgggaacct taccaactac ggcgtttaca cc 52

<210> 40  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence

0219us410-sequence.txt

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

ggtgtaaacg ccgtagttgg taaggttccc acagccctca cccagctca cc

52

15